

WHAT IS CLAIMED IS:

1. An isolated polynucleotide encoding a polypeptide having an amino acid sequence of SEQ ID NO:1 or SEQ ID NO:2.
2. The polynucleotide of claim 1, wherein said polynucleotide has a nucleic acid sequence of SEQ ID NO:3 or a complement thereof.
3. The polynucleotide of claim 2, wherein said polynucleotide further comprises a promoter operable in eukaryotic cells.
4. The polynucleotide of claim 3, wherein said promoter is a heterologous to the coding sequence.
5. The polynucleotide of claim 4, wherein said promoter is selected from the group consisting of hsp68, SV40, CMV, MKC, GAL4_{UAS}, HSV and β-actin.
6. The polynucleotide of claim 5, wherein said promoter is a tissue specific promoter.
7. A nucleic acid of about 15 to about 5000 base pairs comprising from about 15 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
8. The nucleic acid of claim 7, comprising from about 20 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
9. The nucleic acid of claim 7, comprising from about 30 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
10. The nucleic acid of claim 7, comprising from about 50 contiguous base pairs of SEQ ID NO:3, or the complement thereof.

11. The nucleic acid of claim 7, comprising about 100 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
12. The nucleic acid of claim 7, comprising about 150 contiguous base pairs of SEQ ID NO:3.
13. The nucleic acid of claim 7, comprising about 250 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
14. The nucleic acid of claim 7, comprising about 500 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
15. The nucleic acid of claim 7, comprising about 1000 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
16. The nucleic acid of claim 7, comprising about 2500 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
17. The nucleic acid of claim 7, comprising about 3500 contiguous base pairs of SEQ ID NO:3, or the complement thereof.
18. A peptide comprising about 10 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.
19. The peptide of claim 18, comprising about 15 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.
20. The peptide of claim 18, comprising about 20 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.

21. The peptide of claim 18, comprising about 25 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.

22. The peptide of claim 18, comprising about 30 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.

23. The peptide of claim 18, comprising about 50 contiguous amino acids of SEQ ID NO:1 or SEQ ID NO:2.

24. An expression cassette comprising a polynucleotide encoding a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, wherein said polynucleotide is under the control of a promoter operable in eukaryotic cells.

25. The expression cassette of claim 24, wherein said promoter is heterologous to the coding sequence.

26. The expression cassette of claim 25, wherein said promoter is selected from the group consisting of hsp68, SV40, CMV, MKC, GAL4_{UAS}, HSV and β-actin.

27. The expression cassette of claim 25, wherein said promoter is a tissue specific promoter.

28. The expression cassette of claim 25, wherein said promoter is an inducible promoter.

29. The expression cassette of claim 25, wherein said expression cassette is contained in a viral vector.

30. The expression cassette of claim 25, wherein said viral vector is selected from the group consisting of a retroviral vector, an adenoviral vector, and adeno-associated viral vector, a vaccinia viral vector, and a herpesviral vector.

31. The expression cassette of claim 24, wherein said expression cassette further comprises a polyadenylation signal.
32. The expression cassette of claim 24, wherein said expression cassette comprises a second polynucleotide encoding a second polypeptide.
33. The expression cassette of claim 32, wherein said second polynucleotide is under the control of a second promoter.
34. A method for suppressing growth of a cancer cell comprising contacting said cells with an expression cassette comprising a polynucleotide encoding a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, wherein said polynucleotide is under the control of a promoter operable in eukaryotic cells.
35. The method of claim 34, wherein said promoter is heterologous to the polynucleotide sequence.
36. The method of claim 35, wherein said promoter is selected from the group consisting of hsp68, SV40, CMV, MKC, GAL4_{UAS}, HSV and β -actin.
37. The method of claim 35, wherein said promoter is a tissue specific promoter.
38. The method of claim 35, wherein said promoter is an inducible promoter.
39. The method of claim 35, wherein said expression cassette is contained in a viral vector.
40. The method of claim 35, wherein said viral vector is selected from the group consisting of a retroviral vector, an adenoviral vector, and adeno-associated viral vector, a vaccinia viral vector, and a herpesviral vector.

41. The method of claim 34, wherein said expression cassette further comprises a polyadenylation signal.
42. The method of claim 34, wherein said expression cassette comprises a second polynucleotide encoding a second polypeptide.
43. The method of claim 42, wherein said second polynucleotide is under the control of a second promoter.
44. A cell comprising an expression cassette comprising a polynucleotide encoding a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, wherein said polynucleotide is under the control of a promoter operable in eukaryotic cells.
45. A monoclonal antibody that binds immunologically to a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, or an immunologic fragment thereof.
46. The monoclonal antibody of claim 45, wherein the antibody further comprises a detectable label.
47. The monoclonal antibody of claim 46, wherein the label is selected from the group consisting of a fluorescent label, a chemiluminescent label, a radiolabel and an enzyme.
48. A hybridoma cell that produces a monoclonal antibody that binds immunologically to a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, or an immunologic fragment thereof.
49. A polyclonal antisera, antibodies of which bind immunologically to a polypeptide having the sequence of SEQ ID NO:1 or SEQ ID NO:2, or an immunologic fragment thereof.

50. A method of diagnosing a cancer comprising the steps of:

- (i) obtaining a tissue sample from a subject; and
- (ii) assessing the expression of a CAR-1 tumor suppressor in cells of said sample.

51. The method of claim 50, wherein said cancer is selected from the group consisting of brain, lung, liver, spleen, kidney, lymph node, small intestine, pancreas, blood cells, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, esophagus, bone marrow and blood cancer.

52. The method of claim 50, wherein said cancer is colon cancer, kidney cancer or breast cancer.

53. The method of claim 50, wherein said cancer is a carcinoma.

54. The method of claim 50, wherein said brain cancer is a neuroblastoma.

55. The method of claim 50, wherein said sample is a tissue or fluid sample.

56. The method of claim 50, wherein said assessing comprises assaying for a CAR-1-encoding nucleic acid from said sample.

57. The method of claim 56, further comprising subjecting said sample to conditions suitable to amplify said nucleic acid.

58. The method of claim 50, wherein said assessing comprises contacting said sample with an antibody that binds immunologically to a CAR-1 polypeptide.

59. The method of claim 58; further comprising subjecting proteins of said sample to ELISA.

60. The method of claim 50, wherein assessing involves evaluating the level of CAR-1 expression.

61. The method of claim 50, further comprising the step of comparing the expression of CAR-1 with the expression of CAR-1 in non-cancer samples.

62. The method of claim 50, wherein assessing involves evaluating the structure of the CAR-1 gene or transcript.

63. The method of claim 62, wherein said evaluating comprises an assay selected from the group consisting of sequencing, wild-type oligonucleotide hybridization, mutant oligonucleotide hybridization, SSCP, PCR and RNase protection.

64. The method of claim 63, wherein a said evaluating is wild-type or mutant oligonucleotide hybridization and said oligonucleotide is configured in an array on a chip or wafer.

65. A method for altering the phenotype of a tumor cell comprising the step of administering to a cell a tumor suppressor designated CAR-1 under conditions permitting the uptake of said tumor suppressor by said tumor cell.

66. The method of claim 65, wherein said tumor cell is derived from a tissue selected from the group consisting of brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, esophagus, bone marrow and blood tissue.

67. The method of claim 65, wherein the a phenotype is selected from the group consisting of apoptosis, angiogenesis, proliferation, migration, contact inhibition, soft agar growth and cell cycling.

68. The method of claim 65, wherein said tumor suppressor is encapsulated in a liposome.

69. A method for altering the phenotype of a tumor cell comprising the step of contacting the cell with a nucleic acid (i) encoding a tumor suppressor designated CAR-1 and (ii) a promoter active in said tumor cell, wherein said promoter is operably linked to the region encoding said tumor suppressor, under conditions permitting the uptake of said nucleic acid by said tumor cell.

70. The method of claim 69, wherein said tumor cell is derived from a tissue selected from the group consisting of brain, lung, liver, spleen, kidney, lymph node, small intestine,

blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, esophagus, bone marrow and blood tissue.

71. The method of claim 70, wherein the a phenotype is selected from the group consisting of apoptosis, angiogenesis, proliferation, migration, contact inhibition, soft agar growth or cell cycling.
72. The method of claim 70, wherein said nucleic acid is encapsulated in a liposome.
73. The method of claim 70, wherein said nucleic acid is a viral vector selected from the group consisting of retrovirus, adenovirus, adeno-associated virus, vaccinia virus and herpesvirus.
74. The method of claim 73, wherein said nucleic acid is encapsulated in a viral particle.
75. A method for treating subject with cancer comprising the step of administering to said subject a tumor suppressor designated CAR-1.
76. The method of claim 75, wherein said tumor cell is derived from a tissue selected from the group consisting of brain, lung, liver, spleen, kidney, lymph node, small intestine, blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, esophagus, bone marrow and blood tissue.
77. The method of claim 76, wherein the subject is a human.
78. A method for treating a subject with cancer comprising the step of administering to said subject a nucleic acid (i) encoding a tumor suppressor designated CAR-1 and (ii) a promoter active in eukaryotic cells, wherein said promoter is operably linked to the region encoding said tumor suppressor.
79. The method of claim 78, wherein said tumor cell is derived from a tissue selected from the group consisting of brain, lung, liver, spleen, kidney, lymph node, small intestine,

blood cells, pancreas, colon, stomach, breast, endometrium, prostate, testicle, ovary, skin, head and neck, esophagus, bone marrow and blood tissue.

80. The method of claim 78, wherein the subject is a human.
81. A non-human transgenic eukaryote lacking a functional CAR-1 gene.
82. The non-human transgenic eukaryote of claim 81, wherein said eukaryote is a mammal.
83. A non-human transgenic eukaryote that overexpresses CAR-1 as compared to a similar non-transgenic eukaryote.
84. The non-human transgenic eukaryote of claim 83, wherein said eukaryote is a mammal.
85. A method of screening a candidate substance for anti-tumor activity comprising the steps of:
 - (i) providing a cell lacking functional CAR-1 polypeptide;
 - (ii) contacting said cell with said candidate substance; and
 - (iii) determining the effect of said candidate substance on said cell.
86. The method of claim 85, wherein said cell is a tumor cell.
87. The method of claim 86, wherein said tumor cell has a mutation in the coding region of CAR-1.
88. The method of claim 86, wherein said tumor cell has aberrant methylation patterns in the coding region of CAR-1.
89. The method of claim 88, wherein said mutation is a deletion mutant, an insertion mutant, a frameshift mutant, a nonsense mutant, a missense mutant or splice mutant.

90. The method of claim 86, wherein said determining comprises comparing one or more characteristics of the cell in the presence of said candidate substance with characteristics of a cell in the absence of said candidate substance.
91. The method of claim 90, wherein said characteristic is selected from the group consisting of CAR-1 expression, phosphatase activity, proliferation, metastasis, contact inhibition, soft agar growth, cell cycle regulation, tumor formation, tumor progression and tissue invasion.
92. The method of claim 86, wherein said candidate substance is a chemotherapeutic or radiotherapeutic agent.
93. The method of claim 86, wherein said candidate substance is selected from a small molecule library.
94. The method of claim 86, wherein said cell is contacted *in vitro*.
95. The method of claim 86, wherein said cell is contacted *in vivo*.
96. An anti-tumor composition made according to the method comprising the steps of:
 - (i) providing a cell lacking functional CAR-1 polypeptide;
 - (ii) contacting said cell with said candidate substance;
 - (iii) determining the effect of said candidate substance on said cell;
 - (iv) identifying a candidate inhibitor substance; and
 - (v) making said composition.
97. A isolated and purified nucleic acid that hybridizes, under high stringency conditions, to a DNA segment comprising about 15 to 3826 bases of SEQ ID NO:3.
98. The nucleic acid of claim 97, wherein said nucleic acid hybridizes to a DNA segment comprising about 17 to 3826 bases of SEQ ID NO:3.

99. The nucleic acid of claim 97, wherein said nucleic hybridizes to a DNA segment comprising about 20 to 3826 bases of SEQ ID NO:3.

100. The nucleic acid of claim 97, wherein said nucleic hybridizes to a DNA segment comprising about 25 to 3826 bases of SEQ ID NO:3.

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